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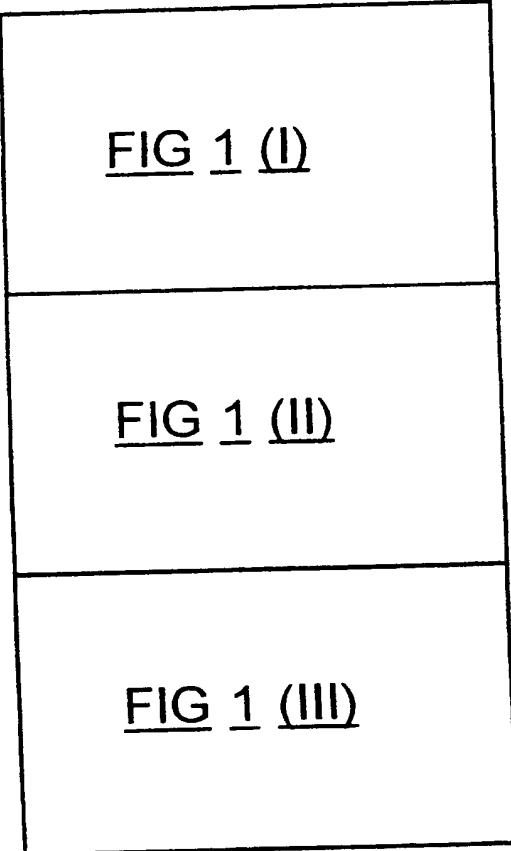


FIG 1 (I)

FIG 1 (II)

FIG 1 (III)

FIG 1

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FIGURE 1 (I)

CAACAGAAGG

TTTAAGTGG

ATCCATTTTC

ATTAGAAAAG

50

96

GCCATCCAT
CAACAGAAGG
TTTAAGTGG
ATCCATTTTC
ATTAGAAAAG
ATCGGACAAA
GGGTACTCTT
AAGCATACAA
C ATG AGG GCG
Met Arg Ala Val Ala
5

GTT TTC TTT GCT TGC GTT CTC TTC TGT ATG GTT CAC AAA GCC
Phe Phe Ala Cys Val Leu Phe Cys Met Val His Lys Ala
10 15

GCA CTT GCG GAT GAT AAA ACG TGC AAC CCT ACA GAT TTT ATG
Ala Leu Ala Asp Asp Lys Thr Cys Asn Pro Thr Asp Phe Met
20 25

GTT ACC CAA ACC ATA ACT GGA TTG ACA ATC GGC GGT AAA CAA
Val Thr Gln Thr Ile Thr G1y Leu Thr Ile G1y G1y Lys Gln
35 40 45

GAG TTC GAG GTC AAT TTA ATA AAC AAT TTG TAT TGT GCA CAA
Glu Phe Glu Val Asn Leu Ile Asn Asn Leu Tyr Cys Ala Gln
50 55 60

264

222

180

138

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FIGURE 1 (II)

TCT	AAT	GTC	AAA	GTT	TCA	TGT	GAC	GGG	CTT	CAT	ACC	ACC	GAA	306	
Ser	Asn	Val	Lys	Val	Ser	Cys	Asp	Gly	Leu	His	Thr	Thr	Glu	75	
65															
CCA	ATA	GAT	CCT	CAC	ATT	ATC	AGA	CCA	CTT	AGT	GAC	GGA	ACG	348	
Pro	Ile	Asp	Pro	His	Ile	Ile	Arg	Pro	Leu	Ser	Asp	Gly	Thr		
AAC	AAC	TGC	CTT	GTC	AAC	AAT	GGA	GCG	CCT	ATT	TCT	CAT	GCT	390	
Asn	Asn	Leu	Val	Val	Asn	Asn	Gly	Ala	Pro	Ile	Ser	His	Ala		
ACT	CTT	GTA	GCA	TTC	AAG	TAT	GCC	TGG	GAT	GTT	CCT	CCA	TCT	432	
Thr	Leu	Val	Ala	Phe	Lys	Tyr	Ala	Trp	Asp	Val	Pro	Pro	Ser		
TTC	AGC	ATC	ATC	AGC	TCT	GAT	ATA	AAT	TGC	TCC	TAA			468	
Phe	Ser	Ile	Ile	Ser	Ser	Asp	Ile	Asn	Cys	Ser	OCH				
														515	
GGAGAAA ATTCTAGTTG GCAGAGAATA ATCATATAGT CTTTTTTACT															

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FIGURE 1 (III)

GAGCTATTAA ATTTCACCAA TTTTCACCAA TAAGATTATT TTAATGGAAT
565
GTTAAATGTTAT TAGAATTGAA AAATAAAAAA AAAAAAAA AAAAAAAA
615
625
AAAAAAA

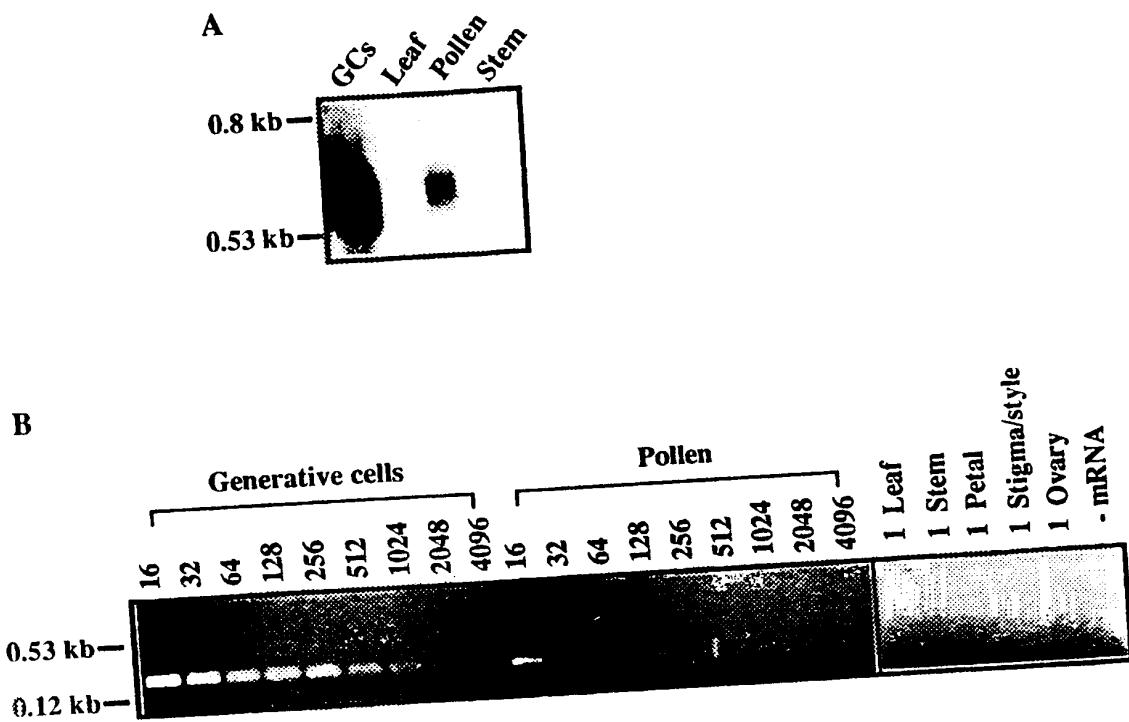


FIG 2

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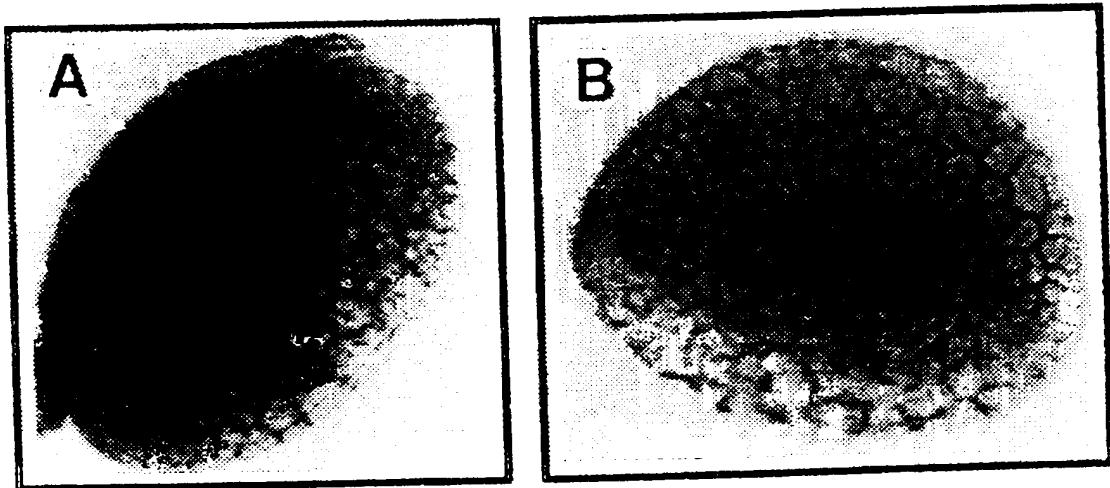


FIG 3

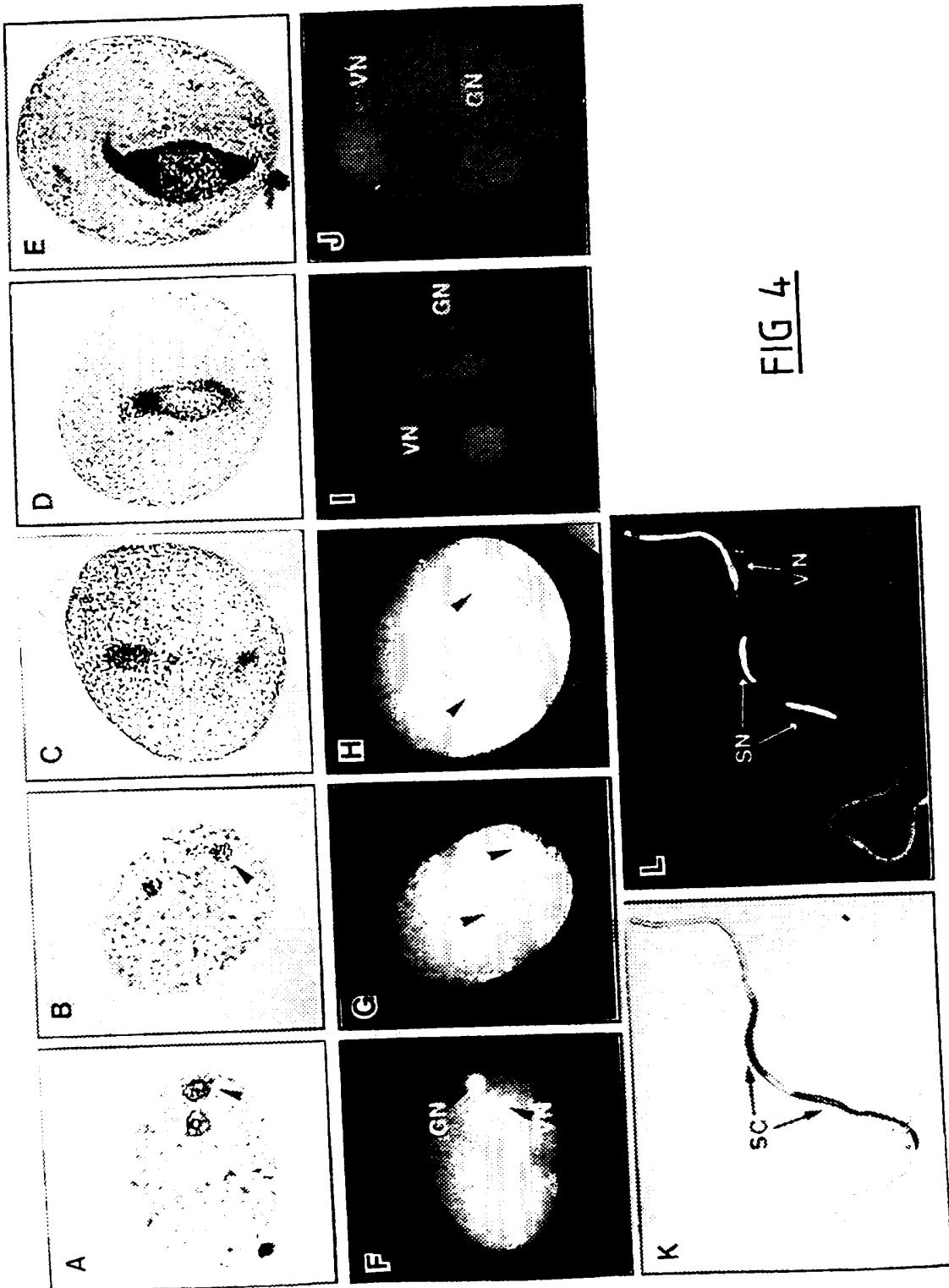


FIG 4

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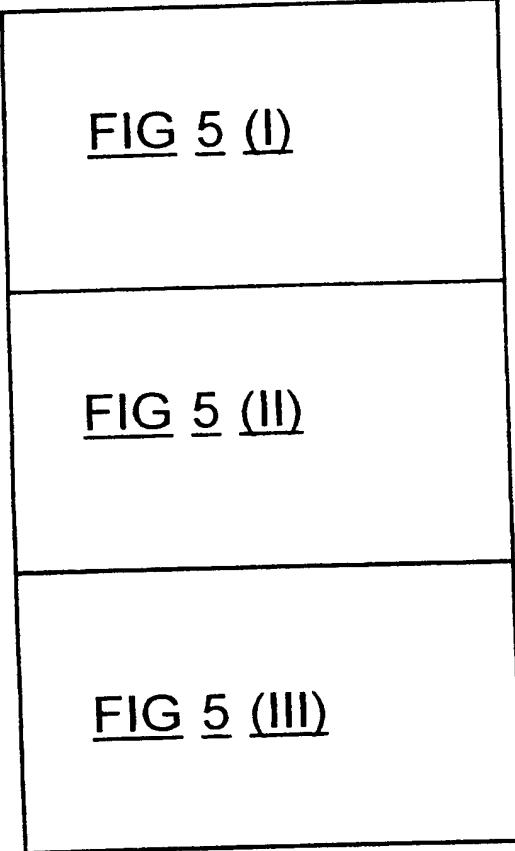


FIG 5 (I)

FIG 5 (II)

FIG 5 (III)

FIG 5

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FIGURE 5 (I)

GAAAGTGGAA	ACATCTCCAT	CAAACCTCTAG	AGTCAGATT	CCCACAAAG	48								
ATG	ATT	TCA	TCG	GCA	AAT	AAC	AAA	GGC	GCC	ACA	AGC	87	
Met	Ile	Ser	Ser	Ala	Asn	Asn	Lys	Gly	Ala	Gly	Thr	Ser	
				5									
CGC	CGC	AAG	CTC	CGT	TCT	GAG	AAG	GCT	GCA	CTC	CAG	TC	126
Arg	Arg	Lys	Leu	Arg	Ser	Glu	Lys	Ala	Ala	Leu	Gln	Phe	
		15				20					25		
TCC	GTC	AGT	CGC	GTC	GAA	TAC	TCC	CTC	AAG	AAG	GGG	CGC	165
Ser	Val	Ser	Arg	Val	Glu	Tyr	Ser	Leu	Lys	Lys	Gly	Arg	
								30		35			
TAT	TGC	AGG	CGC	TTA	GGC	GCT	ACG	GCC	CCC	GTC	TAC	CTA	204
Tyr	Cys	Arg	Arg	Leu	Gly	Ala	Thr	Ala	Pro	Val	Tyr	Leu	
		40				45					50		
GCC	GCC	GTC	CTT	GAA	AAC	CTC	GTG	GCC	GAA	GTG	TTG	GAC	243
Ala	Ala	Ala	Val	Leu	Glu	Asn	Leu	Val	Ala	Glu	Val	Leu	Asp
								55		60		65	

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FIGURE 5 (II)

ATG	GCG	GCG	AAC	GTG	ACA	GAA	GAA	ACA	TCC	CCC	ATT	GTT	282
Met	Ala	Ala	Asn	Val	Thr	Glu	Glu	Thr	Ser	Pro	Ile	Val	
													70
													75
ATC	AAA	CCG	AGG	CAT	ATT	ATG	CTT	GCC	CCC	AGG	AAT	GAT	321
Ile	Lys	Pro	Arg	His	Ile	Met	Leu	Ala	Pro	Arg	Asn	Asp	
													80
GTA	GAA	GTT	GAA	CAA	GCT	GTT	TCA	CGG	TGT	CAC	CAT	CTC	360
Val	Glu	Val	Glu	Gln	Ala	Val	Ser	Arg	Cys	His	His	Leu	
													95
GGC	ATC	AGG	TGT	CGT	CCC	TAAAACACGC	AAAGAGCTGG						398
Gly	Ile	Arg	Cys	Arg	Pro								
													105
ACCGTCGCAA	ACGCCGTTCC	ACCTTTCAGC	CGGATTAGTT	CTTGATATT									448
CATTCTATCA	ATCTTGGTTA	TGTGACTGTG	ATTTTTCGTT	TTGTGTTGAA									498

FIGURE 5 (III)

CTAAGCCCC TAATCTGGAT TTCTCGTTTT ATGTTGAACT AAGTCTGTGC
548
ACTCTTGAAG TAAAAAAA AAAAAAAA AAAAAAAA 587

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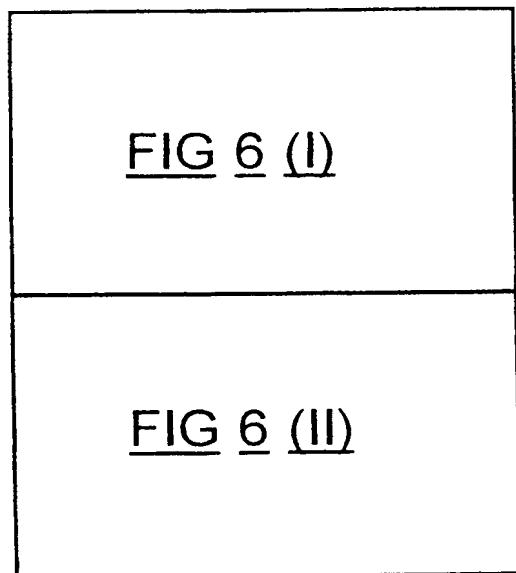


FIG 6

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FIGURE 6 (I)

GATCCAAAT	CATCA	ATG	ACG	ATC	CCC	GAA	AAG	AAA	TCC	GTC	42		
Met	Thr	Ile	Pro	Glu	Lys	Lys	Lys	Ser	Val				
1										5			
GCT	CCG	ATG	GCC	CGT	ATG	AAG	CAT	ACA	GCC	CGC	ATG	TCT	81
Ala	Pro	Met	Ala	Arg	Met	Arg	Met	Lys	His	Thr	Ala	Arg	Met
10													20
ACC	GGC	GGT	AAG	GCT	CCA	CGC	AAG	CAG	CTC	GCC	TCT	AAG	120
Thr	Gly	Gly	Lys	Ala	Pro	Arg	Lys	Gln	Leu	Ala	Ser	Lys	
25													35
GCT	CTT	CGC	AAG	GCG	CCA	CCA	CCA	CCG	ACC	AAA	GGA	GTG	159
Ala	Leu	Arg	Lys	Ala	Pro	Pro	Pro	Pro	Pro	Thr	Lys	Gly	Val
													45
AAG	CAG	CCC	ACC	ACT	ACC	ACC	TCC	GGA	AAA	TGG	CGC	TTC	198
Lys	Gln	Pro	Thr	Thr	Thr	Thr	Ser	Gly	Lys	Trp	Arg	Phe	
50													60

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FIGURE 6 (II)

GGC	AGA	TTT	CAC	AGG	AAA	CTG	CCA	TTC	CAA	GGG	CTG	GTG	237
Ala	Arg	Phe	His	Arg	Lys	Leu	Pro	Phe	Gln	Gly	Leu	Val	
													70
AGG	AAA	ATC	TGG	CAG	GAC	TTG	AAG	ACA	CAT	CTG	CGC	TTC	276
Arg	Lys	Ile	Trp	Gln	Asp	Leu	Lys	Thr	His	Leu	Arg	Phe	
													85
AAG	AAC	CAC	TCG	GTT	CCT	CCA	CTT	GAG	GAG	GTA	ACT	GAG	315
Lys	Asn	His	Ser	Val	Pro	Pro	Leu	Glu	Glu	Val	Thr	Glu	
													90
GTT	TAT	CCT	TGC	CAA	ACT	ATT	GGA	GGA	TGC	TAT			348
Val	Tyr	Pro	Cys	Gln	Thr	Ile	Gly	Gly	Cys	Tyr			
													105
TAGGATATTG AATTGGATA ATGGTTAAAT TATCTGTTCT ACCTTTATGA													398
TCAAATTCT GTGGCTCAGC GTTGTGTAAT TTGGGCAATC GAATTCTTAG													448
CTATATTGCC TCAAAAAAA AAAAAAAAA AAAA													485

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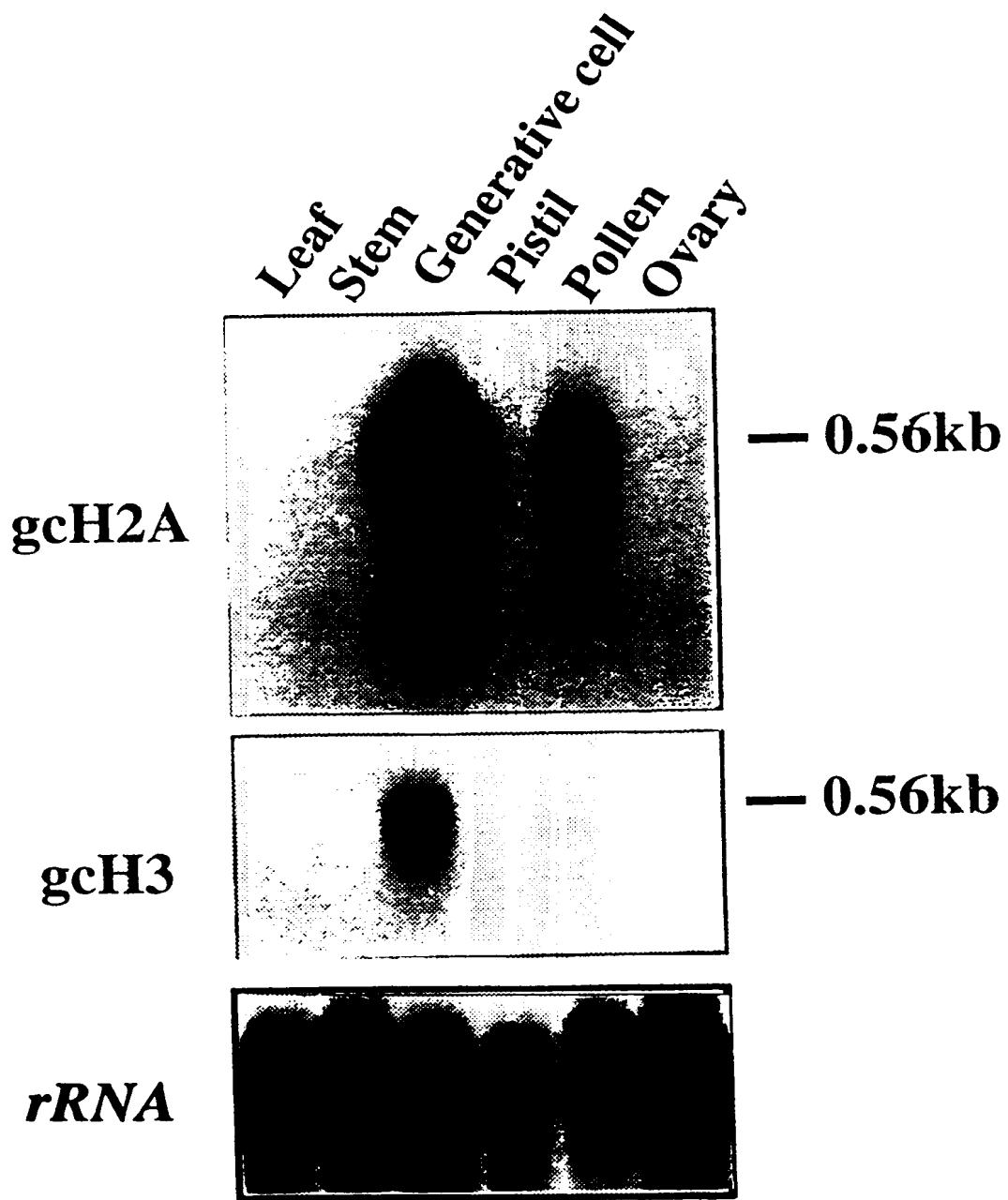


FIG 7

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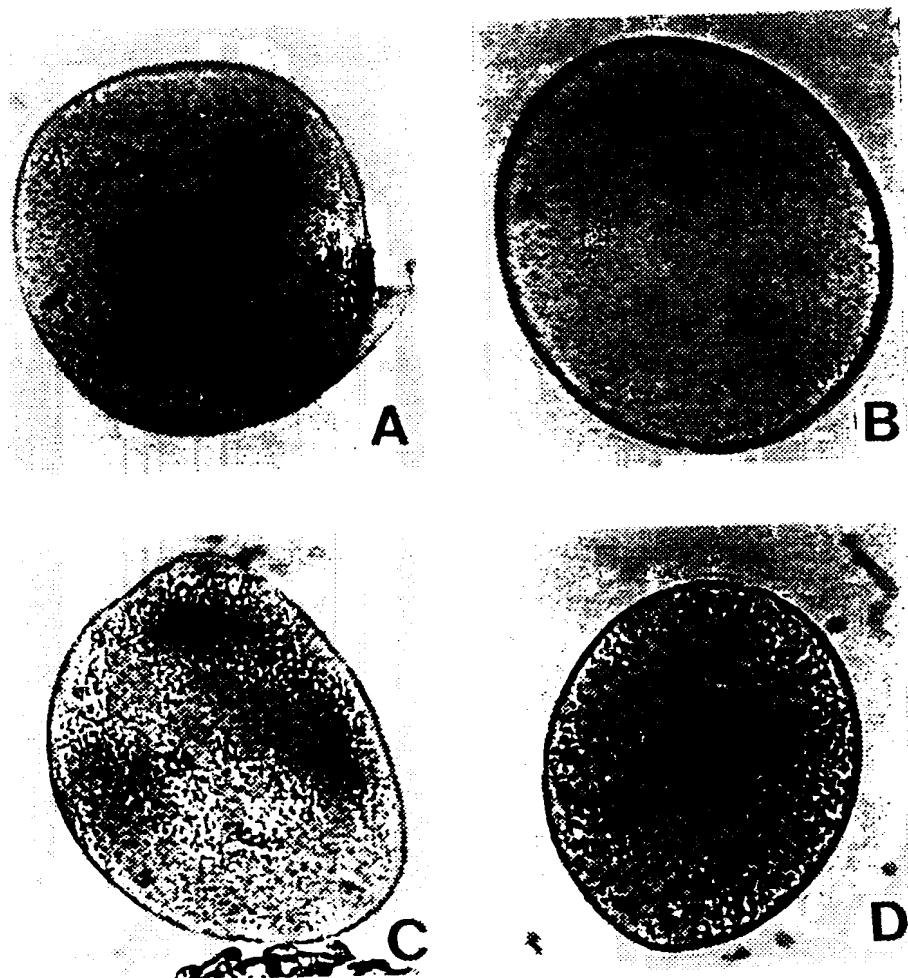


FIG 8

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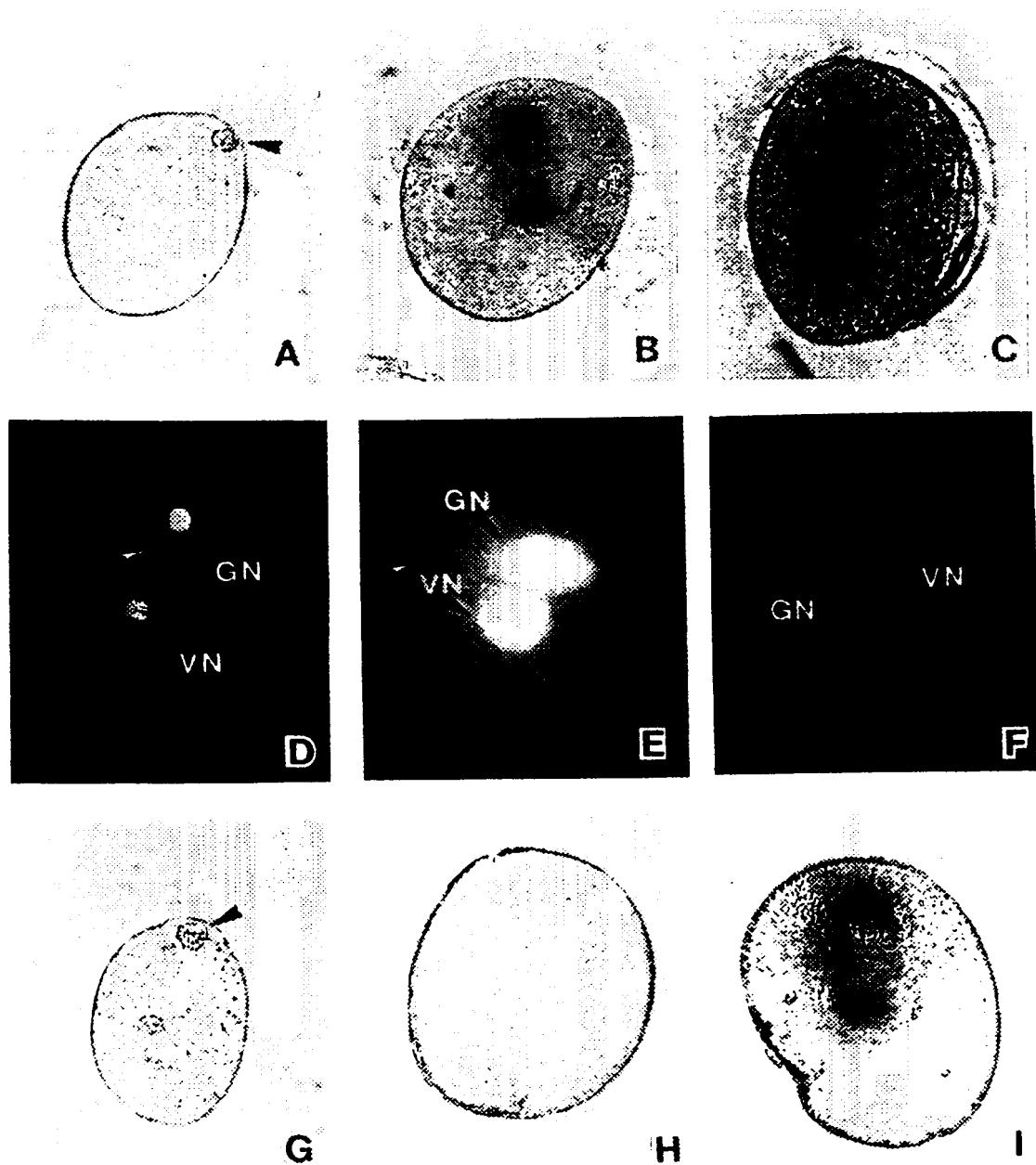


FIG 9

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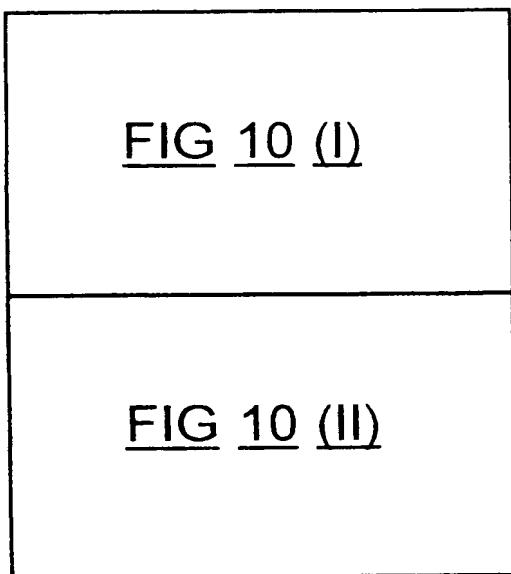


FIG 10

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FIGURE 10 (I)

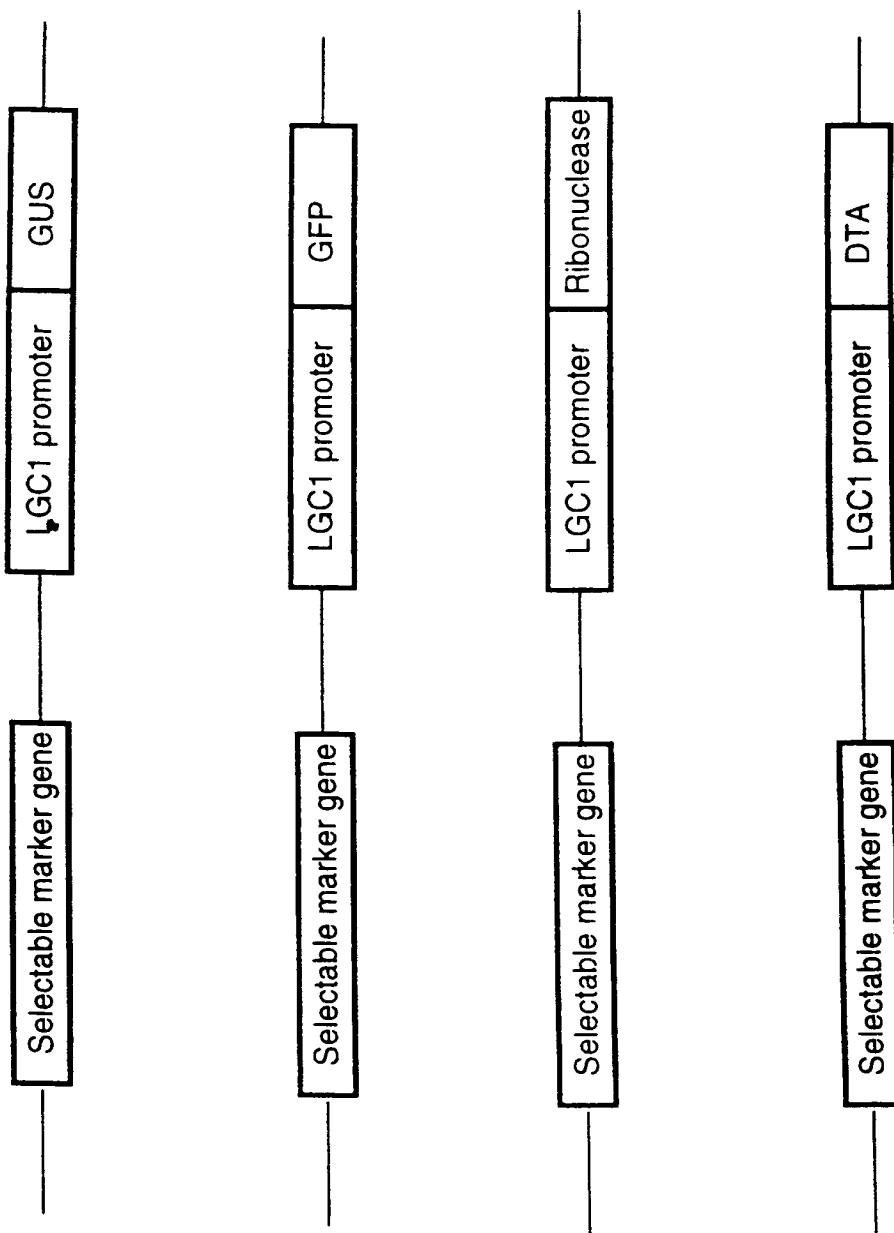
GGAGGGTGT	GGAATTAGGT	TTGCCCTAGG	TTTGCCCTAGG	TTTAGAGAAA	50
TAGTCAAAT	TGTCCTATT	TATAGGCATG	ATTTAGTAGT	GAGTTAATT	100
TCCCTATAATT	TCTCTTCTTG	TATGCTAAA	TAACCTGGTC	TTTAATGAAAT	150
AGATAATTAA	GTTTTGTAGC	AATTCTTCC	TCAAATTGAG	TATCAACAAAT	200
TGTTAGATTG	CTTGGGTGAT	TATATTGAT	ATAATTGTT	GTAAGAAATGT	250
GTAGTGAAGAA	GATTGTGATT	ATTCATTTCG	TTGTGTTGACG	AATTGTTAGA	300
GCCCCATCGC	TAATGCCTTA	TAGTACTCGA	AATATGTTGG	GAATAGAAAGA	350
TGAAAATCC	CATTCTTGT	AGTAGGAGTA	AAAATTGTC	TTTTCAATT	400
TCCATTGAAT	GTAAACCACT	TGCCATTCA	CTGACGGGA	TGGCAGAGTT	450
CCGACCATCT	AGTGATCCGT	GGGATATTGA	TTTTGGTGTG	TCAATGAAAT	500
TGTGAGAACG	GGCTCTGGG	AGAGAAAAGC	CCTCTTGCCT	CTGATATGAA	550
CACTGAGGCT	GATTATGTTA	ACGGATGGAG	ATTATTCAGT	GGCTGAATT	600
GGGTGCTGTA	GAGACAGAAT	TTGAAAGTTC	TAACAAATAAA	CCCTAATTCT	650
GAACCTGGGC	GGGGCTGGGA	TTTTACTCTT	AACGTGAAGA	GAGGCAAGAT	700
GAATTGACAG	CTTGGAAAGTC	GATCCAGTAT	TTGCAGCAGT	CGTGACGAAAT	750

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FIGURE 10 (II)

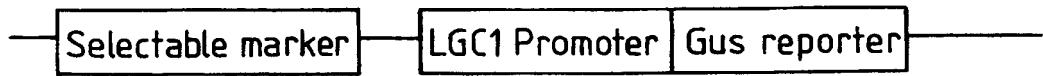
TGGTTGGACA	GTTACATCGG	TCAGAGAATG	CGTTCTATAA	ATTCCCCAA	800
TGGGGCAAGTG	AAAATCCCAT	CCCATCAACA	GAAGTTTTAA	GTGGAAACCC	850
ATTCCAATAG	AGAACGATCGA	ACAAAGGGTA	TTAACACATA	CAA <u>A</u> TGGGG	900
CAGTGGTGT	TCTTTTGCT	TGCCTTCTCT	TCTGTATGGT	TCACAA	945

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FIG 11

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A



B

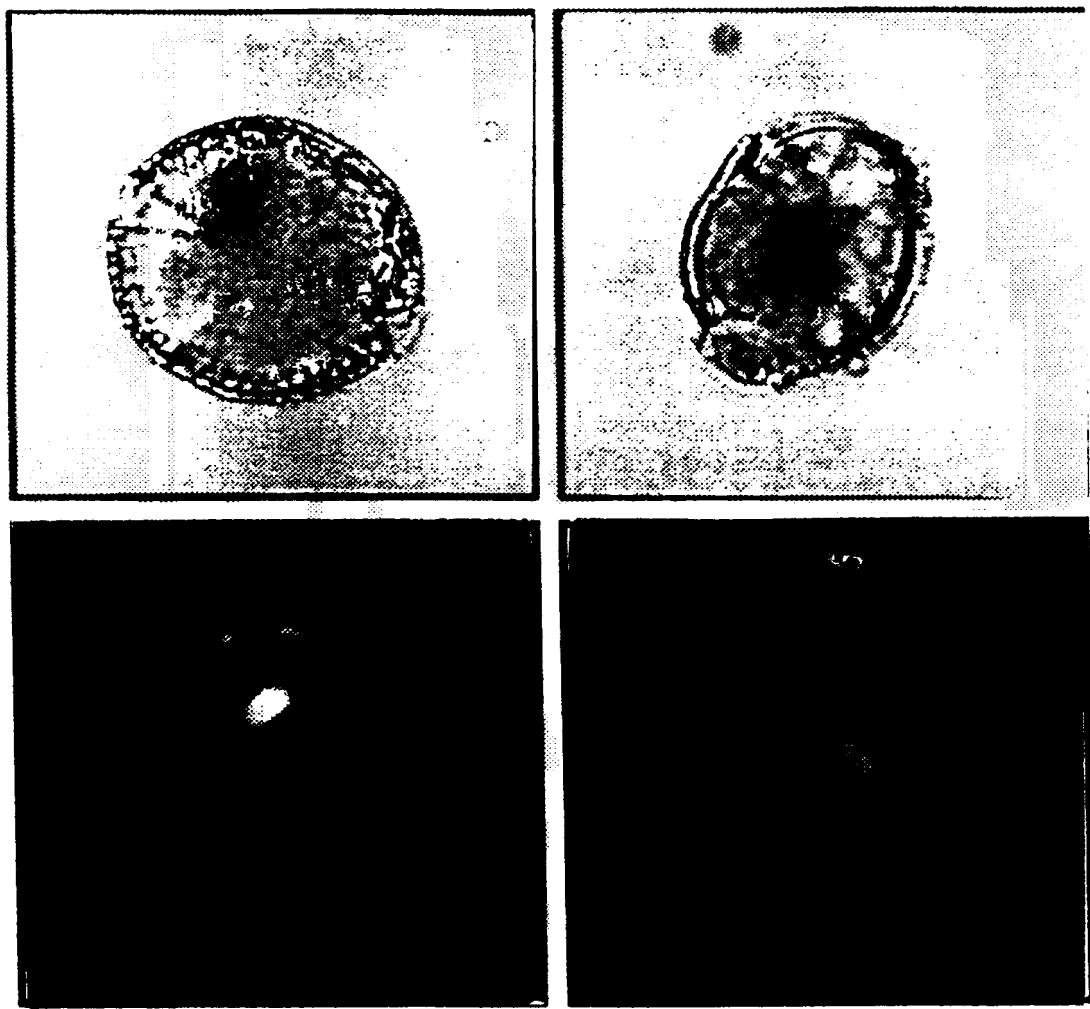


FIG 12